APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/680,208	10/06/2000	Harold A. Robertson	36541-0005	8654

7590   07/10/2002

Mr David J Heller
c/o Ridout & Maybee
Suite 2400
One Queen Street East
Toronto,   M5C 3B1
CANADA

EXAMINER
GOLDBERG, JEANINE ANNE

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 07/10/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER
Jeanine Enewold Goldberg

ART UNIT	PAPER
1655	6

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

The specification contains numerous sequences which are not identified by SEQ ID NO:. Appropriate correction is required.

The disk filed 10/18/00 contains errors. See the raw sequence listing error report.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R.. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jeanine Enewold Goldberg whose telephone number is (703) 306-5817. The examiner can normally be reached on Monday-Friday from 7:00am- 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones can be reached on (703) 308-1152. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

J. Goldberg

W. Gary Jones
Supervisory Patent Examiner
Technology Center 1600

PTO-90C (Rev.3-98)

	Application No.	Applicant(s)
Notice to Comply	09/680,208	ROBERTSON ET AL.
	Examiner	Art Unit	
	Jeanine Enewold Goldberg	1655	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).
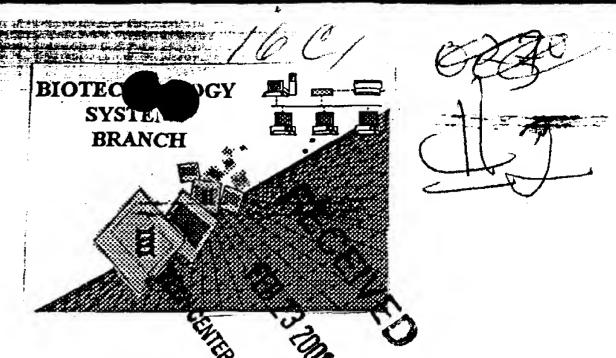
The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
    Technical Assistance.......................................703-287-0200
    To Purchase PatentIn Software........................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING
ERROR REPORT

1633

BIOTECHNOLOGY
SYSTEM
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/680,208*

Source: *OIPE*

Date Processed by STIC: *10-18-00*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

● Sequence Listing Error ● mary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                            This may occur if your file was retrieved in a word processor after creating it.
                            Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                            This may occur if your file was retrieved in a word processor after creating it.
                            Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
        Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                            Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                            As per the rules, each n or Xaa can only represent a single residue.
                            Please present the maximum number of each residue having variable length and
                            indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                            sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                            previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                            to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
                            sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
        (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                            (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                            This sequence is intentionally skipped

                            Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
        (NEW RULES)   **<210> sequence id number**
                            <400> sequence id number
                            000

10 _✓_ Use of n's or **Xaa's**   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or **Xaa**, and which residue n or **Xaa** represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

12 _✓_ Use of <220>Feature   Sequence(s) _//_ are missing the <220>Feature and associated headings.
        (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                            Please explain source of genetic material in <220> to <223> section.
                            (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                            file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                            Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 10/18/2000
PATENT APPLICATION: US/09/680,208   TIME: 17:13:50

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Output Set: N:\CRF3\10182000\I680208.raw

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     7         DENOVAN-WRIGHT, Eileen
     9         NOVANEURON, INC.
    13 <120> TITLE OF INVENTION: GENE NECESSARY FOR STRIATAL FUNCTION, USES THEREOF, AND
    16         COMPOUNDS FOR MODULATING SAME
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C-> 24 <140> CURRENT APPLICATION NUMBER: US/09/680,208
C-> 26 <141> CURRENT FILING DATE: 2000-10-06
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    32 <151> PRIOR FILING DATE: 1999-10-07
    36 <150> PRIOR APPLICATION NUMBER: US60/217,765
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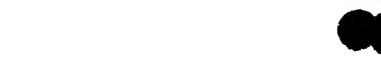
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Does Not Comply
Corrected Diskette Needed
See pp. 6, 7

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RAW SEQUENCE LISTING            DATE: 10/18/2000
PATENT APPLICATION:  US/09/680,208   TIME: 17:13:50

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PATENT APPLICATION: US/09/680,208   TIME: 17:13:50

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290 ctcagtggat gggtctgcag ccaaagcctt aatgggctct cttttgaagg ggaaagaaag 3240
292 aatttcaagc ttatgatatc caatattatt atagttgatg agttagtaaa ttccaaaaaa 3300
294 aaaagatgat tttatatgta tgacataaaa aaaatctttg taaagtgcgc aagtgcaata 3360
296 atttaaagag gtcttatctt tgcatttata aattataaat attgtacatg tgtgtaattt 3420
298 ttcatgtatt catttgcagt ctttgtattt aaaaaaactt tactgttatg tttgtataat 3480
300 agaacattaa tcatttatta taactcagac aaggtgtaaa taaattcata attcaaacag 3540
302 ccagtatata tgcatatatg ggtgttacat tgcaaaaatc tctatctttg ttctattcac 3600
304 atgcttaaag aagtaagaaa tcttttgtgg atatgtaatt atacatataa agtatatata 3660
306 tatgtatgat acatgaaata tatttagaaa tgttcataat tttaatggat attctttggt 3720
308 gtgaataatt gaatacaaca tttttaaaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3780
310 aaaatttttt tttttttttt ttattccaga gattaaagac actagatctt taaccttgaa 3840
312 gggcaggcaa gaggtcggca atgctgtcaa catagaagtc agggaccatt ttcttcttga 3900
314 acatgcagtc actttcctga ttgctcttca catcctcaag gctccggaat tccgggggtg 3960
316 tggtgggctt tgatctcagg actctggagg cagaagcagg cagatctctg tgaatatgag 4020
```

RAW SEQUENCE LISTING   DATE: 10/18/2000
PATENT APPLICATION: US/09/680,208   TIME: 17:13:50

Input Set : A:\HD GENE.txt
Output Set: N:\CRF3\10182000\I680208.raw

```
318 gccagcctgc actacacaga gctccagacc agtcatggct acatcatgaa accctgtctc 4080
320 aaaaagaaaa taaaaactgt tgtgtttcta ccatagtgtt aaactcagag tctgagtaat 4140
322 gtcgggctga catgctcggg tgtttaacat accttcagct ttgacgaggc gctgaacagt 4200
324 caaagtctgg ccttggggag cggtggctgt gtttgtgctc aagtccaccg tgaaatcctg 4260
326 attgtgaatt tggacaaccg tgtccttctt cttggccttc catgcaacct ccaacttcat 4320
328 gttggtcatt ttgtcaaaac actgtgtgat gtttttatca atatactgcc attccacata 4380
330 tgtagagatg tagtctgcct ggctttcctt ttctttagcc aatcgaatgc tcttgatcat 4440
332 gccctcaatc tcatctctag cttttatcac gtctctgcta attcctgaaa cttgaatcga 4500
334 agttttcttc tggttcatct caatggtgat gttcagttcc ttctgaatct cattcagttt 4560
336 ctcgtactcc tccatgtcaa agtcactgac acactcatcg tcattggtgt aggaaagctg 4620
338 ctctttggta atcagttcct ttagccagga gattgttttg ttcacactgt ctacccctga 4680
340 accacatacc tggaaaactg tgtgctctat tttcttttcc aaaaccaggg tgttcttttt 4740
342 gggggaagct tgcttgggaa agccaagaaa ggctaaagag aaaatggaaa ttaatgtttc 4800
344 ttttactccc ttcaacatca aggttaggaa tatgtatttc ataaaagcta acaactcaca 4860
346 ggcaatctta gacatcactg actgcttggc aggcgactgc ttggggggag ctggagagcc 4920
348 ttctctttct ttcatgttgt cgtaaaaaaa ttgcagaata tggggctgga agataacaac 4980
350 tttaactctc ttcacagcct gcactgattt tttctggaca aattcttcaa tggcatctat 5040
352 tatcgctttt gctactacgt ttgggtcctg ttgagcattt ccttcaaaaa caaaaaaagc 5100
354 acatttttaa aaagtcaagg ttaagatcca cctgcaaaaa aaagctgcaa tataagcgag 5160
356 gaattctagt tgtcacagga aataaaaatg tctgttccca ctataatcaa tgtagactga 5220
358 taatattatg ccagcaaata gttttgaagt cctaggcaca gtgggaggag gttttgttcc 5280
360 acgctgttca taagccaata ccccagcaaa agaccttaaa ggacaacttg taatttggga 5340
362 cattcacatc tgtcctcttc atctgatctg gctcccagtg tcactctcta acacggtcct 5400
364 tagagggaca atttatccct gcctctgctt gatcttatgc atgtatctgt attcttccag 5460
366 ccatccctgg cgacctgatt tttctaaggc acccaaaact gtaagctact tcttataatc 5520
368 tataattctg agcatattag ttagcctgag cctccaggat atctttcttc cctatactca 5580
370 gtccagtttt agctgcccag aaggattcaa agctgatcta cgagtagatc actcctgtct 5640
372 acagcttgtt ccagatcttg tttctcaagc cctggaagcc atcagccagg taagattgta 5700
374 aaacaatccc tttctaatca tgggtgtggc ccaaagtgaa tggccggaat tc         5752
378 <210> SEQ ID NO: 3
380 <211> LENGTH: 475
382 <212> TYPE: DNA
381 <213> ORGANISM: mouse
388 <400> SEQUENCE: 3
390 tgtatgggaa tagtgtttcc atatgatctg ttgtctggag tatatgctac atgttcattt 60
392 actgtacaaa aacccagtgc agctgatgat gcaaagcagt ctctctctgt gtacagtgcc 120
394 ccacctattt aaaaatcacg tacttgccca gaacactgtg aaacacttaa cataagaaca 180
396 aacgcagcgt ctggattctt tccaaggaga gcagctttct ccacaggaac acagtaacaa 240
398 aagaggtccg ccgccatcca cacccagcca agacacctca gaggccatag ggacaacctc 300
400 cttgctggcc aacacctgct ggagcagggg cacaggtccc agcaactgat cctcagtgga 360
402 tgggtctgca gccaaagcct taatgggctc tcttttgaag gggaaagaaa gaatttcaag 420
404 cttatgatat ccaatattat tatagttgat gagttagtaa attccaaaaa aaaaa   475
408 <210> SEQ ID NO: 4
410 <211> LENGTH: 20
412 <212> TYPE: DNA
414 <213> ORGANISM: Artificial Sequence
418 <220> FEATURE:
420 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
424 <400> SEQUENCE: 4
```

RAW SEQUENCE LISTING   DATE: 10/18/2000
PATENT APPLICATION: US/09/680,208   TIME: 17:13:50

Input Set : A:\HD GENE.txt
Output Set: N:\CRF3\10182000\I680208.raw

```
426 agggctgtca atcatgctgg                                          20
430 <210> SEQ ID NO: 5
432 <211> LENGTH: 20
434 <212> TYPE: DNA
436 <213> ORGANISM: Artificial Sequence
440 <220> FEATURE:
442 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
446 <400> SEQUENCE: 5
448 aaactcacgg tcggtgcagc                                          20
452 <210> SEQ ID NO: 6
454 <211> LENGTH: 24
456 <212> TYPE: DNA
458 <213> ORGANISM: Artificial Sequence
462 <220> FEATURE:
464 <223> OTHER INFORMATION: Description of Artificial Sequence:probe
468 <400> SEQUENCE: 6
470 attaaccctc actaaatgct gtat                                     24
474 <210> SEQ ID NO: 7
476 <211> LENGTH: 30
478 <212> TYPE: DNA
480 <213> ORGANISM: Artificial Sequence
484 <220> FEATURE:
486 <223> OTHER INFORMATION: Description of Artificial Sequence:probe
490 <400> SEQUENCE: 7
492 cattatgctg agtgatatct tttttttttcg                              30
496 <210> SEQ ID NO: 8
498 <211> LENGTH: 38
500 <212> TYPE: DNA
502 <213> ORGANISM: Artificial Sequence
506 <220> FEATURE:
508 <223> OTHER INFORMATION: Description of Artificial Sequence:probe
512 <400> SEQUENCE: 8
514 gaacatgtag catatactcc agacaacaga tcatatgg                      38
518 <210> SEQ ID NO: 9
520 <211> LENGTH: 32
522 <212> TYPE: DNA
524 <213> ORGANISM: Artificial Sequence
528 <220> FEATURE:
530 <223> OTHER INFORMATION: Description of Artificial Sequence:probe
534 <400> SEQUENCE: 9
536 cagcttctcc acaggaacac agtaacaaag ag                            32
540 <210> SEQ ID NO: 10
542 <211> LENGTH: 35
544 <212> TYPE: DNA
546 <213> ORGANISM: Artificial Sequence
550 <220> FEATURE:
552 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
556 <400> SEQUENCE: 10
558 ctatttcaca agagactgac cagccaataa atctc                         35
```

<210> 11

<211> 7581

<212> DNA

<213> Unknown

Seq #11 (small segment shown)

——> *Missing mandatory <220>, <223> features to explain the "Unknown" sequence. See #12 on Error Summary Sheet.*

<400> 11

```
ggtaaaaaaa aagcatgtga atnntaacaa cntctanant ntcncngnat gttatggcag 3420
aattttagtc acgtccaaaa caaaaagatt attccagaag atacctcatc ctatgcctga 3480
aaggctccac agcatggcgt ccgtctccca gggttctgat ccgtctcctc acggtgcaat 3540
caggcaggac agagaggagg gctgcagggc taccacattg acccagaagg tatctcctct 3600
caccattcag acatccataa ggaatgccaa atgctgtatt gaatagttct ctgtgtgact 3660
ttctagagaa gccaggacac cctgagcctt tccngggaa ctctaaggag tcacaggttc 3720
```

Missing mandatory <220> to <223> features to explain "n's" in the sequence See #10 on Error Summary Sheet. Please check __entire__ sequence for "n's" and explain each instance.

<210> 12

<211> 7618

<212> DNA

<213> mouse

<400> 12

Seq #12 (small segment shown)

missing mandatory <220> to <223> features to explain "n's" in the sequence. See #16 on Error Summary sheet. Please check entire sequence for "n's" and explain each instance

```
tgccccacct atttaaaaat cacgtacaan cccagaacac tgtgaaacac ttaacataag 6840
aaacaaacgc agcgtctgga ttctttccaa ggagagcagc tttctccaca ggaacacagt 6900
aacaaaagag gtccgccgcc atccacaccc agccaagaca cctcagaggc catagggaca 6960
acctccttgc tggccaacac ctgctggagc agggcacagg tcccagcaac tgatcctcag 7020
tggatgggtc cgcagtcaaa gccttaatgg gctctctttt gaaggggaaa gaaanntttc 7080
```

VERIFICATION SUMMARY   DATE: 10/18/2000
PATENT APPLICATION: US/09/680,208   TIME: 17:13:51

Input Set : **A:\HD GENE.txt**
Output Set: **N:\CRF3\10182000\I680208.raw**

```
L:24 M:270 C: Current Application Number differs, Replaced Application Number
L:26 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:572 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:572 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:678 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:678 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:678 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:686 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:686 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:696 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:696 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:800 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:800 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:808 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:808 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1068 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:1068 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:1068 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:1068 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:1068 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:1076 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:1076 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:1076 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:1076 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
M:340 Repeated in SeqNo=12
```